SCORE Search Results Details for Application 10797393 and Search Result 20070118_073132_us-10-797-393a-1.rag.

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This page gives you Search Results detail for the Application 10797393 and Search Result 20070118_073132_us-10-797-393a-1.rag.

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OM protein - protein search, using sw model

Run on:          January 18, 2007, 09:03:27 ; Search time 197 Seconds
                                            (without alignments)
                                            1123.313 Million cell updates/sec

Title:           US-10-797-393A-1
Perfect score:   2585
Sequence:        1 LSAASWRTQSIYFLLTDRFG.........PASVVDSSSLCGGSGRLYVE 484

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters:      2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        A_Geneseq_8:*
                 1:  geneseqp1980s:*
                 2:  geneseqp1990s:*
                 3:  geneseqp2000s:*
                 4:  geneseqp2001s:*
                 5:  geneseqp2002s:*
                 6:  geneseqp2003as:*
                 7:  geneseqp2003bs:*
                 8:  geneseqp2004s:*
                 9:  geneseqp2005s:*
                 10: geneseqp2006s:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                SUMMARIES

                 %
Result           Query
   No.    Score  Match Length DB  ID                      Description
 ------------------------------------------------------------------------
```



```
     1    2585  100.0    484  5  AAE24207                 Aae24207 Aspergill
     2    2585  100.0    484  8  ADS75939                 Ads75939 Aspergill
     3    2585  100.0    484  9  ADV09273                 Adv09273 Aspergill
     4    2585  100.0    484  9  AEB72807                 Aeb72807 Fungal ac
     5    2585  100.0    484  9  AEC92136                 Aec92136 Protein s
     6    2585  100.0    484  10  AEE27539                 Aee27539 Fungal ac
     7    2544   98.4    476  9  ADY52195                 Ady52195 Aspergill
     8    2540   98.3    476  9  ADY52228                 Ady52228 Aspergill
     9    2538   98.2    476  9  ADY52230                 Ady52230 Aspergill
    10    2537   98.1    476  9  ADY52232                 Ady52232 Aspergill
    11    2537   98.1    476  9  ADY52231                 Ady52231 Aspergill
    12    2536   98.1    476  9  ADY52233                 Ady52233 Aspergill
    13    2536   98.1    476  9  ADY52227                 Ady52227 Aspergill
    14    2536   98.1    476  9  ADY52229                 Ady52229 Aspergill
    15    2503   96.8    505  9  ADW25838                 Adw25838 Aspergill
    16    2503   96.8    505  9  AED43752                 Aed43752 A. niger
    17  2501.5   96.8    477  9  ADY52234                 Ady52234 Aspergill
    18    2483   96.1    511  9  ADW25804                 Adw25804 A. niger
    19    2483   96.1    588  9  AEB72843                 Aeb72843 Hybrid al
    20    2483   96.1    608  9  AEB72839                 Aeb72839 Hybrid al
    21    2483   96.1    609  9  ADW25834                 Adw25834 Hybrid al
    22    2483   96.1    619  9  AEB72837                 Aeb72837 Hybrid al
    23    2483   96.1    629  9  ADW25830                 Adw25830 Hybrid al
    24    2483   96.1    640  9  ADW25828                 Adw25828 Hybrid al
    25    2436   94.2    480  10  AEE61224                 Aee61224 A. kawach
    26    2436   94.2    480  10  AEF57528                 Aef57528 A. kawach
    27    2436   94.2    619  10  AEE61223                 Aee61223 A. kawach
    28    2436   94.2    619  10  AEF57522                 Aef57522 A. kawach
    29    2436   94.2    640  10  AEE61214                 Aee61214 A. kawach
    30    2436   94.2    640  10  AEF57523                 Aef57523 A. kawach
    31    2427   93.9    640  9  ADW21552                 Adw21552 Aspergill
    32    2427   93.9    640  9  ADW25837                 Adw25837 Aspergill
    33    2427   93.9    640  9  AEB72835                 Aeb72835 Wild type
    34    2420   93.6    619  9  AED94831                 Aed94831 Aspergill
    35    2420   93.6    640  9  AED94832                 Aed94832 Aspergill
    36  1940.5   75.1    630  6  ABB80178                 Abb80178 A. fumiga
    37    1846   71.4    608  9  ADW25847                 Adw25847 Hybrid al
    38    1842   71.3    608  9  ADW25851                 Adw25851 Hybrid al
    39    1839   71.1    608  9  ADW25846                 Adw25846 Hybrid al
    40    1834   70.9    608  9  ADW25852                 Adw25852 Hybrid al
    41    1830   70.8    608  9  ADW25853                 Adw25853 Hybrid al
    42    1826   70.6    608  9  ADW25843                 Adw25843 Hybrid al
    43    1821   70.4    608  9  ADW25854                 Adw25854 Hybrid al
    44    1818   70.3    608  9  ADW25849                 Adw25849 Hybrid al
    45    1817   70.3    608  9  ADW25848                 Adw25848 Hybrid al

                              ALIGNMENTS

RESULT 1
AAE24207
ID   AAE24207 standard; protein; 484 AA.
XX
AC   AAE24207;
XX
DT   04-OCT-2002  (first entry)
XX
DE   Aspergillus niger alpha-amylase protein.
XX
KW   Ethanol production; starch; fermentation; liquefaction; alpha-amylase;
KW   fuel alcohol; fuel additive; neutral spirit; industrial ethanol; enzyme.
XX
OS   Aspergillus niger.
XX
```

```
PN   WO200238787-A2.
XX
PD   16-MAY-2002.
XX
PF   09-NOV-2001; 2001WO-DK000737.
XX
PR   10-NOV-2000; 2000DK-00001676.
PR   21-NOV-2000; 2000US-0252213P.
PR   11-DEC-2000; 2000DK-00001854.
PR   15-DEC-2000; 2000US-0256015P.
XX
PA   (NOVO ) NOVOZYMES AS.
PA   (NOVO ) NOVOZYMES NORTH AMERICA INC.
XX
PI   Veit C, Felby C, Fuglsang CC;
XX
DR   WPI; 2002-479793/51.
XX
PT   Producing ethanol from starch-containing material e.g., tubers, roots,
PT   whole grain, for use in fuel, by fermentation comprises carrying out a
PT   secondary liquefaction step in the presence of a thermostable acid alpha-
PT   amylase.
XX
PS   Claim 35; Page 31-33; 33pp; English.
XX
CC   The invention relates to a method for producing ethanol from starch-
CC   containing material, by fermentation. The method involves carrying out a
CC   secondary liquefaction step in the presence of a thermostable acid alpha-
CC   amylase. The method is used in producing ethanol from a starch-containing
CC   material such as tubers, roots or whole grain (e.g. corn, wheat or barley
CC   or their combination) or combination of the materials. Preferably ethanol
CC   is produced from starch-containing material that is obtained from cereals
CC   or from corns, cobs, wheat, barley, rye, milo and potatoes or their
CC   combination. The ethanol produced by above mentioned method is used as
CC   fuel alcohol and/or fuel additive. The ethanol is also useful as drinking
CC   ethanol i.e., potable neutral spirits or industrial ethanol. The present
CC   sequence is Aspergillus niger alpha-amylase protein
XX
SQ   Sequence 484 AA;

  Query Match             100.0%;  Score 2585;  DB 5;  Length 484;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-198;
  Matches  484;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LSAASWRTQSIYFLLTDRFGRTDNSTTATCNTGNEIYCGGSWQGIIDHLDYIEGMGFTAI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LSAASWRTQSIYFLLTDRFGRTDNSTTATCNTGNEIYCGGSWQGIIDHLDYIEGMGFTAI 60

Qy         61 WISPITEQLPQDTADGEAYHGYWQQKIYDVNSNFGTADNLKSLSDALHARGMYLMVDVVP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISPITEQLPQDTADGEAYHGYWQQKIYDVNSNFGTADNLKSLSDALHARGMYLMVDVVP 120

Qy        121 DHMGYAGNGNDVDYSVFDPFDSSSYFHPYCLITDWDNLTMVEDCWEGDTIVSLPDLDTTE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DHMGYAGNGNDVDYSVFDPFDSSSYFHPYCLITDWDNLTMVEDCWEGDTIVSLPDLDTTE 180

Qy        181 TAVRTIWYDWVADLVSNYSVDGLRIDSVLEVQPDFFPGYNKASGVYCVGEIDNGNPASDC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TAVRTIWYDWVADLVSNYSVDGLRIDSVLEVQPDFFPGYNKASGVYCVGEIDNGNPASDC 240

Qy        241 PYQKVLDGVLNYPIYWQLLYAFESSSGSISNLYNMIKSVASDCSDPTLLGNFIENHDNPR 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PYQKVLDGVLNYPIYWQLLYAFESSSGSISNLYNMIKSVASDCSDPTLLGNFIENHDNPR 300

Qy        301 FAKYTSDYSQAKNVLSYIFLSDGIPIVYAGEEQHYAGGKVPYNREATWLSGYDTSAELYT 360
```



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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FAKYTSDYSQAKNVLSYIFLSDGIPIVYAGEEQHYAGGKVPYNREATWLSGYDTSAELYT 360

Qy        361 WIATTNAIRKLAIAADSAYITYANDAFYTDSNTIAMAKGTSGSQVITVLSNKGSSGSSYT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WIATTNAIRKLAIAADSAYITYANDAFYTDSNTIAMAKGTSGSQVITVLSNKGSSGSSYT 420

Qy        421 LTLSGSGYTSGTKLIEAYTCTSVTVDSSGDIPVPMASGLPRVLLPASVVDSSSLCGGSGR 480
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Db        421 LTLSGSGYTSGTKLIEAYTCTSVTVDSSGDIPVPMASGLPRVLLPASVVDSSSLCGGSGR 480

Qy        481 LYVE 484
              ||||
Db        481 LYVE 484


RESULT 2
ADS75939
ID   ADS75939 standard; protein; 484 AA.
XX
AC   ADS75939;
XX
DT   16-DEC-2004  (first entry)
XX
DE   Aspergillus niger acid alpha-amylase for ethanol production method.
XX
KW   enzyme; alcohol; slurry; water; granular starch; acid alpha-amylase;
KW   glucoamylase; gelatinization; yeast; beer; fuel ethanol; potable ethanol;
KW   industrial ethanol.
XX
OS   Aspergillus niger.
XX
PN   WO2004080923-A2.
XX
PD   23-SEP-2004.
XX
PF   10-MAR-2004; 2004WO-DK000154.
XX
PR   10-MAR-2003; 2003US-0453326P.
XX
PA   (NOVO ) NOVOZYMES AS.
XX
PI   Olsen HS, Pedersen S, Festersen RM;
XX
DR   WPI; 2004-677503/66.
XX
PT   Production of alcohol product, e.g. beer, comprises holding slurry of
PT   water and granular starch in presence of acid alpha-amylase and
PT   glucoamylase followed by simultaneous saccharification and fermentation.
XX
PS   Claim 9; SEQ ID NO 1; 43pp; English.
XX
CC   The invention relates to a method for the production of an alcohol
CC   product by holding a slurry of water and granular starch in the presence
CC   of an acid alpha-amylase and a glucoamylase at 0-20 deg C below the
CC   initial gelatinization temperature of the granular starch; holding the
CC   slurry in the presence of acid alpha-amylase, glucoamylase and yeast at
CC   10-35 deg C to produce ethanol; and optionally recovering the ethanol.
CC   The method is used for the production of an alcohol product such as beer
CC   or recovered ethanol, e.g. fuel ethanol, potable ethanol or industrial
CC   ethanol. This sequence represents an acid fungal alpha-amylase from
CC   Aspergillus niger used in the method of the invention.
XX
SQ   Sequence 484 AA;
```

```
  Query Match           100.0%;  Score 2585;  DB 8;  Length 484;
  Best Local Similarity  100.0%;  Pred. No. 3.9e-198;
  Matches  484;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LSAASWRTQSIYFLLTDRFGRTDNSTTATCNTGNEIYCGGSWQGIIDHLDYIEGMGFTAI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LSAASWRTQSIYFLLTDRFGRTDNSTTATCNTGNEIYCGGSWQGIIDHLDYIEGMGFTAI 60

Qy         61 WISPITEQLPQDTADGEAYHGYWQQKIYDVNSNFGTADNLKSLSDALHARGMYLMVDVVP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISPITEQLPQDTADGEAYHGYWQQKIYDVNSNFGTADNLKSLSDALHARGMYLMVDVVP 120

Qy        121 DHMGYAGNGNDVDYSVFDPFDSSSYFHPYCLITDWDNLTMVEDCWEGDTIVSLPDLDTTE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DHMGYAGNGNDVDYSVFDPFDSSSYFHPYCLITDWDNLTMVEDCWEGDTIVSLPDLDTTE 180

Qy        181 TAVRTIWYDWVADLVSNYSVDGLRIDSVLEVQPDFFPGYNKASGVYCVGEIDNGNPASDC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TAVRTIWYDWVADLVSNYSVDGLRIDSVLEVQPDFFPGYNKASGVYCVGEIDNGNPASDC 240

Qy        241 PYQKVLDGVLNYPIYWQLLYAFESSSGSISNLYNMIKSVASDCSDPTLLGNFIENHDNPR 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PYQKVLDGVLNYPIYWQLLYAFESSSGSISNLYNMIKSVASDCSDPTLLGNFIENHDNPR 300

Qy        301 FAKYTSDYSQAKNVLSYIFLSDGIPIVYAGEEQHYAGGKVPYNREATWLSGYDTSAELYT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FAKYTSDYSQAKNVLSYIFLSDGIPIVYAGEEQHYAGGKVPYNREATWLSGYDTSAELYT 360

Qy        361 WIATTNAIRKLAIAADSAYITYANDAFYTDSNTIAMAKGTSGSQVITVLSNKGSSGSSYT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WIATTNAIRKLAIAADSAYITYANDAFYTDSNTIAMAKGTSGSQVITVLSNKGSSGSSYT 420

Qy        421 LTLSGSGYTSGTKLIEAYTCTSVTVDSSGDIPVPMASGLPRVLLPASVVDSSSLCGGSGR 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LTLSGSGYTSGTKLIEAYTCTSVTVDSSGDIPVPMASGLPRVLLPASVVDSSSLCGGSGR 480

Qy        481 LYVE 484
              ||||
Db        481 LYVE 484


RESULT 3
ADV09273
ID   ADV09273 standard; protein; 484 AA.
XX
AC   ADV09273;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Aspergillus niger acid alpha-amylase amino acid sequence - SEQ ID 1.
XX
KW   alcohol production ; starch hydrolysis; fuel ethanol; potable ethanol;
KW   industrial ethanol; enzyme; acid alpha-amylase.
XX
OS   Aspergillus niger.
XX
PN   WO2004106533-A1.
XX
PD   09-DEC-2004.
XX
PF   28-MAY-2004; 2004WO-DK000373.
XX
PR   30-MAY-2003; 2003DK-00000812.
XX
PA   (NOVO ) NOVOZYMES AS.
```



```
XX
PI   Olsen HS,  Norman BE,  Wuempelmann M,  Tams JW;
XX
DR   WPI; 2005-021301/02.
XX
PT   Producing an alcohol product, e.g. ethanol, comprises holding slurry at
PT   elevated temperature below the initial gelatinization temperature of the
PT   granular starch followed by saccharification and fermentation.
XX
PS   Claim 9; SEQ ID NO 1; 43pp; English.
XX
CC   The invention comprises a method for producing an alcohol product. The
CC   method involves holding a slurry of water and granular starch below the
CC   initial gelatinization temperature of the granular starch, and fermenting
CC   the slurry with a yeast to produce ethanol (where both steps are
CC   performed in the presence of an acid alpha-amylase, a maltose generating
CC   enzyme and an alpha-glucosidase). The method of the invention is useful
CC   in the hydrolysis of granular starch or a starch hydrolysis process. The
CC   method of the invention is useful for producing an alcohol product (e.g.
CC   fuel ethanol, potable ethanol and/or industrial ethanol). The present
CC   amino acid sequence represents an Aspergillus niger alpha-amylase of the
CC   invention.
XX
SQ   Sequence 484 AA;

  Query Match           100.0%;  Score 2585;  DB 9;  Length 484;
  Best Local Similarity  100.0%;  Pred. No. 3.9e-198;
  Matches  484;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LSAASWRTQSIYFLLTDRFGRTDNSTTATCNTGNEIYCGGSWQGIIDHLDYIEGMGFTAI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LSAASWRTQSIYFLLTDRFGRTDNSTTATCNTGNEIYCGGSWQGIIDHLDYIEGMGFTAI 60

Qy         61 WISPITEQLPQDTADGEAYHGYWQQKIYDVNSNFGTADNLKSLSDALHARGMYLMVDVVP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISPITEQLPQDTADGEAYHGYWQQKIYDVNSNFGTADNLKSLSDALHARGMYLMVDVVP 120

Qy        121 DHMGYAGNGNDVDYSVFDPFDSSSYFHPYCLITDWDNLTMVEDCWEGDTIVSLPDLDTTE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DHMGYAGNGNDVDYSVFDPFDSSSYFHPYCLITDWDNLTMVEDCWEGDTIVSLPDLDTTE 180

Qy        181 TAVRTIWYDWVADLVSNYSVDGLRIDSVLEVQPDFFPGYNKASGVYCVGEIDNGNPASDC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TAVRTIWYDWVADLVSNYSVDGLRIDSVLEVQPDFFPGYNKASGVYCVGEIDNGNPASDC 240

Qy        241 PYQKVLDGVLNYPIYWQLLYAFESSSGSISNLYNMIKSVASDCSDPTLLGNFIENHDNPR 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PYQKVLDGVLNYPIYWQLLYAFESSSGSISNLYNMIKSVASDCSDPTLLGNFIENHDNPR 300

Qy        301 FAKYTSDYSQAKNVLSYIFLSDGIPIVYAGEEQHYAGGKVPYNREATWLSGYDTSAELYT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FAKYTSDYSQAKNVLSYIFLSDGIPIVYAGEEQHYAGGKVPYNREATWLSGYDTSAELYT 360

Qy        361 WIATTNAIRKLAIAADSAYITYANDAFYTDSNTIAMAKGTSGSQVITVLSNKGSSGSSYT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WIATTNAIRKLAIAADSAYITYANDAFYTDSNTIAMAKGTSGSQVITVLSNKGSSGSSYT 420

Qy        421 LTLSGSGYTSGTKLIEAYTCTSVTVDSSGDIPVPMASGLPRVLLPASVVDSSSLCGGSGR 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LTLSGSGYTSGTKLIEAYTCTSVTVDSSGDIPVPMASGLPRVLLPASVVDSSSLCGGSGR 480

Qy        481 LYVE 484
              ||||
Db        481 LYVE 484
```

```
RESULT 4
AEB72807
ID   AEB72807 standard; protein; 484 AA.
XX
AC   AEB72807;
XX
DT   06-OCT-2005  (first entry)
XX
DE   Fungal acid alpha-amylase.
XX
KW   glucoamylase; fermentation; cereals; alcohol; ethanol; fuel ethanol;
KW   potable ethanol; industrial ethanol; gelatinization.
XX
OS   Aspergillus niger.
XX
PN   WO2005069840-A2.
XX
PD   04-AUG-2005.
XX
PF   14-JAN-2005; 2005WO-US001147.
XX
PR   16-JAN-2004; 2004US-0537071P.
PR   14-DEC-2004; 2004US-0636013P.
XX
PA   (NOVO ) NOVOZYMES NORTH AMERICA INC.
PA   (NOVO ) NOVOZYMES AS.
XX
PI   Allain E, Wenger KS, Bisgard-Frantzen H;
XX
DR   WPI; 2005-542205/55.
XX
PT   Producing fermentation product e.g. ethanol from starch-containing
PT   material involves saccharifying the material with specific glucoamylase,
PT   at temperature below initial gelatinization temperature of the material
PT   and fermenting.
XX
PS   Disclosure; SEQ ID NO 3; 96pp; English.
XX
CC   This sequence represents an acid alpha-amylase which was used in the
CC   method of the invention. The method for producing a fermentation product
CC   from milled starch-containing material involves: saccharifying milled
CC   starch-containing material with the glucoamylase from the fungi Athelia
CC   rolfsii, at temperature below the initial gelatinization temperature of
CC   starch containing material; and fermenting using a fermenting medium. The
CC   process is carried out for 1 - 250, especially 80 - 130 hours, at pH of 3
CC   - 7, especially 4 - 5. The dry solid (DS) content in the process is 20 -
CC   55 (preferably 25 - 40, especially 30 - 35) wt.%. The sugar concentration
CC   is kept below 3 wt.% during saccharification and fermentation. A slurry
CC   of water and milled starch-containing material is prepared before step
CC   (a). The milled-starch-containing material is prepared by milling starch-
CC   containing material to a particle size of 0.1 - 0.5 mm. The
CC   saccharification is carried out simultaneously. The fermentation is
CC   carried out at 28 - 36, especially 32 deg C. The glucoamylase is present
CC   in an amount of 0.01 - 10, especially 0.1 - 0.5 AGU/g DS. The
CC   fermentation product is recovered after fermentation. The process is
CC   carried out in the presence of a protease (preferably acid protease,
CC   especially fungal acid protease). The starch-containing material is
CC   obtained from tubers, roots, stems, seeds or whole grains of corn, cobs,
CC   wheat, barley, rye, milo, sago, cassava, manioc, tapioca, sorghum, rice
CC   or potatoes (preferably cereals). The method of the invention is for
CC   producing a fermentation product e.g. alcohol such as ethanol selected
CC   from fuel ethanol, potable ethanol and industrial ethanol. The method
CC   produces fermentation product without gelatinization of the starch-
CC   containing material; and produces ethanol in higher yield.
```



```
XX
SQ   Sequence 484 AA;

  Query Match             100.0%;  Score 2585;  DB 9;  Length 484;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-198;
  Matches  484;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LSAASWRTQSIYFLLTDRFGRTDNSTTATCNTGNEIYCGGSWQGIIDHLDYIEGMGFTAI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LSAASWRTQSIYFLLTDRFGRTDNSTTATCNTGNEIYCGGSWQGIIDHLDYIEGMGFTAI 60

Qy         61 WISPITEQLPQDTADGEAYHGYWQQKIYDVNSNFGTADNLKSLSDALHARGMYLMVDVVP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 DHMGYAGNGNDVDYSVFDPFDSSSYFHPYCLITDWDNLTMVEDCWEGDTIVSLPDLDTTE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DHMGYAGNGNDVDYSVFDPFDSSSYFHPYCLITDWDNLTMVEDCWEGDTIVSLPDLDTTE 180

Qy        181 TAVRTIWYDWVADLVSNYSVDGLRIDSVLEVQPDFFPGYNKASGVYCVGEIDNGNPASDC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TAVRTIWYDWVADLVSNYSVDGLRIDSVLEVQPDFFPGYNKASGVYCVGEIDNGNPASDC 240

Qy        241 PYQKVLDGVLNYPIYWQLLYAFESSSGSISNLYNMIKSVASDCSDPTLLGNFIENHDNPR 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PYQKVLDGVLNYPIYWQLLYAFESSSGSISNLYNMIKSVASDCSDPTLLGNFIENHDNPR 300

Qy        301 FAKYTSDYSQAKNVLSYIFLSDGIPIVYAGEEQHYAGGKVPYNREATWLSGYDTSAELYT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FAKYTSDYSQAKNVLSYIFLSDGIPIVYAGEEQHYAGGKVPYNREATWLSGYDTSAELYT 360

Qy        361 WIATTNAIRKLAIAADSAYITYANDAFYTDSNTIAMAKGTSGSQVITVLSNKGSSGSSYT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WIATTNAIRKLAIAADSAYITYANDAFYTDSNTIAMAKGTSGSQVITVLSNKGSSGSSYT 420

Qy        421 LTLSGSGYTSGTKLIEAYTCTSVTVDSSGDIPVPMASGLPRVLLPASVVDSSSLCGGSGR 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LTLSGSGYTSGTKLIEAYTCTSVTVDSSGDIPVPMASGLPRVLLPASVVDSSSLCGGSGR 480

Qy        481 LYVE 484
              ||||
Db        481 LYVE 484


RESULT 5
AEC92136
ID   AEC92136 standard; protein; 484 AA.
XX
AC   AEC92136;
XX
DT   01-DEC-2005  (first entry)
XX
DE   Protein sequence of alpha amylase B.
XX
KW   alpha-amylase B; fermentation; cereal; ethanol; sugar; oligosaccharide.
XX
OS   Aspergillus niger.
XX
PN   WO2005092015-A2.
XX
PD   06-OCT-2005.
XX
PF   18-MAR-2005; 2005WO-US009218.
XX
PR   19-MAR-2004; 2004US-0554615P.
```

```
PR   28-MAY-2004; 2004US-0575133P.
XX
PA   (NOVO ) NOVOZYMES NORTH AMERICA INC.
PA   (NOVO ) NOVOZYMES AS.
XX
PI   Bhargava S,  Bisgard-Frantzen H,  Frisner H,  Vikso-Nielsen A;
PI   Johal M;
XX
DR   WPI; 2005-676933/69.
XX
PT   Liquefying starch-containing material by treating the starch-containing
PT   material with a bacterial alpha-amylase at set temperatures and for a
PT   defined period of time.
XX
PS   Claim 15; SEQ ID NO 1; 30pp; English.
XX
CC   The new invention relates to a method of liquefying starch-containing
CC   material by treating the material with a bacterial alpha-amylase at a
CC   temperature around 70-90 degrees C for 15-90 minutes, and treating the
CC   material with an alpha-amylase at a temperature between 60-80 degrees C
CC   for 30-90 minutes. Also claimed are a process of producing a fermentation
CC   product from starch-containing material by fermentation; and a process of
CC   producing syrup from starch-containing material. The starch-containing
CC   material comprises tubers, roots and/or whole grain, obtained from
CC   cereals such as corn, cob, wheat, barley, rye, milo and/or potatoes. The
CC   bacterial alpha-amylase is derived from Bacillus stearothermophilus alpha
CC   -amylase or a variant with the mutations: I181+G182 especially
CC   I181+G182+N193F. The alpha-amylase is an acid alpha-amylase, preferably
CC   an acid fungal alpha-amylase, preferably derived from Aspergillus niger
CC   or Aspergillus oryzae. The acid alpha-amylase is SEQ ID NO: 1. The method
CC   further comprises recovering the fermentation product, which is ethanol.
CC   The methods are useful for producing syrup from starch-containing
CC   material. The syrup is glucose, maltose, fructose syrups, malto-
CC   oligosaccharides or isomalto-oligosaccharides. The method is useful in
CC   liquefying starch-containing material for producing a fermentation
CC   product, preferably ethanol, or syrup, preferably glucose, maltose,
CC   fructose syrups, malto-oligosaccharides or isomalto-oligosaccharides. The
CC   preent sequence is the protein sequence of alpha amylase B.
XX
SQ   Sequence 484 AA;

  Query Match             100.0%;  Score 2585;  DB 9;  Length 484;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-198;
  Matches  484;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LSAASWRTQSIYFLLTDRFGRTDNSTTATCNTGNEIYCGGSWQGIIDHLDYIEGMGFTAI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LSAASWRTQSIYFLLTDRFGRTDNSTTATCNTGNEIYCGGSWQGIIDHLDYIEGMGFTAI 60

Qy         61 WISPITEQLPQDTADGEAYHGYWQQKIYDVNSNFGTADNLKSLSDALHARGMYLMVDVVP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISPITEQLPQDTADGEAYHGYWQQKIYDVNSNFGTADNLKSLSDALHARGMYLMVDVVP 120

Qy        121 DHMGYAGNGNDVDYSVFDPFDSSSYFHPYCLITDWDNLTMVEDCWEGDTIVSLPDLDTTE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DHMGYAGNGNDVDYSVFDPFDSSSYFHPYCLITDWDNLTMVEDCWEGDTIVSLPDLDTTE 180

Qy        181 TAVRTIWYDWVADLVSNYSVDGLRIDSVLEVQPDFFPGYNKASGVYCVGEIDNGNPASDC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TAVRTIWYDWVADLVSNYSVDGLRIDSVLEVQPDFFPGYNKASGVYCVGEIDNGNPASDC 240

Qy        241 PYQKVLDGVLNYPIYWQLLYAFESSSGSISNLYNMIKSVASDCSDPTLLGNFIENHDNPR 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PYQKVLDGVLNYPIYWQLLYAFESSSGSISNLYNMIKSVASDCSDPTLLGNFIENHDNPR 300
```



```
Qy        301 FAKYTSDYSQAKNVLSYIFLSDGIPIVYAGEEQHYAGGKVPYNREATWLSGYDTSAELYT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FAKYTSDYSQAKNVLSYIFLSDGIPIVYAGEEQHYAGGKVPYNREATWLSGYDTSAELYT 360

Qy        361 WIATTNAIRKLAIAADSAYITYANDAFYTDSNTIAMAKGTSGSQVITVLSNKGSSGSSYT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WIATTNAIRKLAIAADSAYITYANDAFYTDSNTIAMAKGTSGSQVITVLSNKGSSGSSYT 420

Qy        421 LTLSGSGYTSGTKLIEAYTCTSVTVDSSGDIPVPMASGLPRVLLPASVVDSSSLCGGSGR 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LTLSGSGYTSGTKLIEAYTCTSVTVDSSGDIPVPMASGLPRVLLPASVVDSSSLCGGSGR 480

Qy        481 LYVE 484
              ||||
Db        481 LYVE 484


RESULT 6
AEE27539
ID   AEE27539 standard; protein; 484 AA.
XX
AC   AEE27539;
XX
DT   09-FEB-2006  (first entry)
XX
DE   Fungal acid alpha-amylase B protein sequence.
XX
KW   fermentation; ethanol; fuel; acid alpha-amylase;
KW   1,4-alpha-D-glucan glucanohydrolase; enzyme; E.C 3.2.1.1.
XX
OS   Aspergillus niger.
XX
PN   WO2005113785-A2.
XX
PD   01-DEC-2005.
XX
PF   11-MAY-2005; 2005WO-US016390.
XX
PR   13-MAY-2004; 2004US-0570727P.
PR   01-DEC-2004; 2004US-0632201P.
PR   03-DEC-2004; 2004US-0633293P.
XX
PA   (NOVO ) NOVOZYMES NORTH AMERICA INC.
PA   (NOVO ) NOVOZYMES AS.
XX
PI   Bhargava S,  Frisner H,  Bisgard-Frantzen H,  Tams JW;
XX
DR   WPI; 2006-010609/01.
DR   SWISSPROT; P56271.
XX
PT   Producing a fermentation product (preferably ethanol) from a starch-
PT   containing material, comprises treatment with alpha-amylase, and then
PT   alpha-glucosidase, before fermentation with a fermenting organism.
XX
PS   Claim 11; SEQ ID NO 1; 54pp; English.
XX
CC   The new invention relates to a method of producing (M1) a fermentation
CC   product from starch-containing materials. The method comprises subjecting
CC   starch-containing material to an alpha-amylase, subjecting the obtained
CC   material to an alpha-glucosidase and optionally a glucose-generating
CC   and/or maltose-generating enzyme, and fermenting the material in the
CC   presence of a fermenting organism. In (M1), the fermentation product is
CC   recovered after fermentation, preferably by distillation. (M1) is useful
CC   for producing a fermentation product from starch-containing materials,
CC   where the fermentation product is ethanol, which is useful as e.g. fuel
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CC   ethanol, drinking ethanol (such as potable neutral spirits), or
CC   industrial ethanol, including fuel additive. The present sequence is a
CC   fungal acid alpha amylase B (FAAB), (1,4-alpha-D-glucan
CC   glucanohydrolase).
XX
SQ   Sequence 484 AA;

  Query Match             100.0%;  Score 2585;  DB 10;  Length 484;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-198;
  Matches  484;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LSAASWRTQSIYPLLTDRPGRTDNSTTATCNTGNEIYCGGSWQGIIDHLDYIEGMGFTAI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LSAASWRTQSIYFLLTDRPGRTDNSTTATCNTGNEIYCGGSWQGIIDHLDYIEGMGFTAI 60

Qy         61 WISPITEQLPQDTADGEAYHGYWQQKIYDVNSNFGTADNLKSLSDALHARGMYLMVDVVP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISPITEQLPQDTADGEAYHGYWQQKIYDVNSNFGTADNLKSLSDALHARGMYLMVDVVP 120

Qy        121 DHMGYAGNGNDVDYSVFDPFDSSSYFHPYCLITDWDNLTMVEDCWEGDTIVSLPDLDTTE 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DHMGYAGNGNDVDYSVFDPFDSSSYFHPYCLITDWDNLTMVEDCWEGDTIVSLPDLDTTE 180

Qy        181 TAVRTIWYDWVADLVSNYSVDGLRIDSVLEVQPDFFPGYNKASGVYCVGEIDNGNPASDC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TAVRTIWYDWVADLVSNYSVDGLRIDSVLEVQPDFFPGYNKASGVYCVGEIDNGNPASDC 240

Qy        241 PYQKVLDGVLNYPIYWQLLYAFESSSGSISNLYNMIKSVASDCSDPTLLGNFIENHDNPR 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PYQKVLDGVLNYPIYWQLLYAFESSSGSISNLYNMIKSVASDCSDPTLLGNFIENHDNPR 300

Qy        301 FAKYTSDYSQAKNVLSYIFLSDGIPIVYAGEEQHYAGGKVPYNREATWLSGYDTSAELYT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FAKYTSDYSQAKNVLSYIFLSDGIPIVYAGEEQHYAGGKVPYNREATWLSGYDTSAELYT 360

Qy        361 WIATTNAIRKLAIAADSAYITYANDAFYTDSNTIAMAKGTSGSQVITVLSNKGSSGSSYT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 WIATTNAIRKLAIAADSAYITYANDAFYTDSNTIAMAKGTSGSQVITVLSNKGSSGSSYT 420

Qy        421 LTLSGSGYTSGTKLIEAYTCTSVTVDSSGDIPVPMASGLPRVLLPASVVDSSSLCGGSGR 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LTLSGSGYTSGTKLIEAYTCTSVTVDSSGDIPVPMASGLPRVLLPASVVDSSSLCGGSGR 480

Qy        481 LYVE 484
              ||||
Db        481 LYVE 484


RESULT 7
ADY52195
ID   ADY52195 standard; protein; 476 AA.
XX
AC   ADY52195;
XX
DT   19-MAY-2005  (first entry)
XX
DE   Aspergillus niger alpha-amylase.
XX
KW   alpha amylase; hydrolysis; starch; bread; anti-staling; enzyme.
XX
OS   Aspergillus niger.
XX
PN   WO2005019443-A2.
XX
PD   03-MAR-2005.
```



```
XX
PF   23-AUG-2004; 2004WO-DK000558.
XX
PR   22-AUG-2003; 2003DK-00001201.
XX
PA   (NOVO ) NOVOZYMES AS.
XX
PI   Svendsen A,  Beier L,  Vind J,  Spendler T,  Jensen MT;
XX
DR   WPI; 2005-202646/21.
XX
PT   Producing fungal alpha-amylase variants which is useful for preparing
PT   dough or baked from dough product, based on comparison of three-
PT   dimensional structures of fungal alpha-amylase and maltogenic alpha-
PT   amylase.
XX
PS   Claim 11; SEQ ID NO 3; 26pp; English.
XX
CC   The invention relates to a method of producing a variant fungal alpha-
CC   amylase by superimposing a three-dimensional (3D) model for a fungal
CC   alpha-amylase and a 3D model for a maltogenic alpha-amylase, selecting an
CC   amino acid residue in the fungal amylase which has a C-alpha atom located
CC   greater than 0.8 Angstrom from the C-alpha atom of amino acid residue in
CC   the maltogenic alpha-amylase and less than 11 Angstrom from an atom of an
CC   enzyme substrate, altering the fungal amylase sequence, and producing the
CC   variant polypeptide. Also described are (i) a polypeptide comprising (a)
CC   an amino acid sequence having at least 70% identity to a fully defined
CC   478 amino acids (SEQ ID No:2) sequence given in the specification, and
CC   compared to SEQ ID No:2 comprises an amino acid alteration which is a
CC   deletion, substitution or insertion at a position corresponding to 15, 32
CC   -36, 63-64, 73-77, 119-120, 125-126, 151-152, 155-156, 167-172, 211 or
CC   233-239, and has the ability to hydrolyze starch, (b) has an amino acid
CC   sequence having at least 70% identity to a fully defined 476 amino acids
CC   (SEQ ID No:3) sequence given in the specification, compared to SEQ ID
CC   No:3 comprises an amino acid alteration which comprises Q35K, Q35R, P70K,
CC   L151F, L151D, N233G+G234D, D75G, D75A or 166-171 (Glu-Gly-Asp-Thr-Ile-
CC   Val) substituted with Phe-Thr-Asp-Pro-Ala-Gly-Phe, and has the ability to
CC   hydrolyze starch, or (c) has an amino acid sequence having at least 70%
CC   identity to a fully defined 475 amino acids (SEQ ID No:4) sequence given
CC   in the specification, compared to SEQ ID No:4 comprises an amino acid
CC   alteration which comprises G35K, G35R, A76deletion+D77deletion,
CC   D74deletion+A78deletion, D74A, D74G, D77A, D77G, Y157W or
CC   L168F+A169T+T171P+P172A+T173G, and has the ability to hydrolyze starch.
CC   The method of the invention is useful for producing a variant fungal
CC   alpha-amylase. The polypeptide produced by the method is useful for
CC   preparing a dough, or a product baked from dough. The polypeptide of the
CC   method is useful for anti-staling in baked products. The variant
CC   polypeptide has improved anti-staling effect and a higher degree of exo-
CC   amylase activity. This sequence represents Aspergillus niger alpha-
CC   amylase.
XX
SQ   Sequence 476 AA;

  Query Match             98.4%;  Score 2544;  DB 9;  Length 476;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-195;
  Matches  476;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LSAASWRTQSIYPLLTDRFGRTDNSTTATCNTGNEIYCGGSWQGIIDHLDYIEGMGFTAI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LSAASWRTQSIYFLLTDRFGRTDNSTTATCNTGNEIYCGGSWQGIIDHLDYIEGMGFTAI 60

Qy         61 WISPITEQLPQDTADGEAYHGYWQQKIYDVNSNFGTADNLKSLSDALHARGMYLMVDVVP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WISPITEQLPQDTADGEAYHGYWQQKIYDVNSNFGTADNLKSLSDALHARGMYLMVDVVP 120
```

SCORE Search Results Details for Application 10797393 and Search Result 20070118_073134_us-10-797-393a-1.rup.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Suggestions

This page gives you Search Results detail for the Application 10797393 and Search Result 20070118_073134_us-10-797-393a-1.rup.

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                    GenCore version 5.1.9
                Copyright (c) 1993 - 2007  Biocceleration Ltd.


OM protein - protein search, using sw model

Run on:         January 18, 2007, 09:04:22 ; Search time 303 Seconds
                                           (without alignments)
                                           1477.583 Million cell updates/sec

Title:          US-10-797-393A-1
Perfect score:  2585
Sequence:       1 LSAASWRTQSIYFLLTDRFG.........PASVVDSSSLCGGSGRLYVE 484

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters:      2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       UniProt_7.2:*
                1:  uniprot_sprot:*
                2:  uniprot_trembl:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                SUMMARIES
                 %
Result           Query
   No.   Score  Match Length DB  ID                      Description
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     1    2585  100.0    484  1  AMYA_ASPNG              P56271 aspergillus
     2    2427   93.9    640  2  O13296_ASPKA            O13296 aspergillus
     3  2390.5   92.5    634  2  Q76L96_ASPAW            Q76196 aspergillus
     4  1940.5   75.1    630  2  Q4WIT5_ASPFU            Q4wit5 aspergillus
     5    1780   68.9    499  2  Q7LV45_ASPPL            Q7lv45 aspergillus
     6    1780   68.9    499  2  Q96TH4_ASPOR            Q96th4 aspergillus
     7    1778   68.8    498  2  Q76CT3_ASPKA            Q76ct3 aspergillus
     8    1778   68.8    499  1  AMYA_ASPOR              P10529 aspergillus
```



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     9    1778   68.8    499  2  Q2U6K7_ASPOR            Q2u6k7 aspergillus
    10    1774   68.6    499  2  Q76L99_ASPAW            Q76l99 aspergillus
    11    1772   68.5    499  1  AMYB_ASPAW              Q02906 aspergillus
    12    1771   68.5    498  1  AMYA_ASPAW              Q02905 aspergillus
    13    1769   68.4    499  1  AMY_ASPSH               P30292 aspergillus
    14  1701.5   65.8    494  2  Q4WPQ9_ASPFU            Q4wpq9 aspergillus
    15    1670   64.6    623  2  Q9UV09_EMENI            Q9uv09 emericella
    16    1670   64.6    623  2  Q5B7S8_EMENI            Q5b7s8 aspergillus
    17    1578   61.0    490  2  Q9UV07_EMENI            Q9uv07 emericella
    18    1578   61.0    490  2  Q5BBR2_EMENI            Q5bbr2 aspergillus
    19    1453   56.2    647  2  Q6YF33_LIPST            Q6yf33 lipomyces s
    20    1425   55.1    624  1  AMY1_LIPKO              Q01117 lipomyces k
    21    1387   53.7    507  1  AMY2_DEBOC              Q08806 debaryomyce
    22  1304.5   50.5    512  1  AMY1_DEBOC              P19269 debaryomyce
    23  1291.5   50.0    494  1  AMY1_SACFI              P21567 saccharomyc
    24    1247   48.2    631  2  Q92394_9HETE            Q92394 cryptococcu
    25    1151   44.5    561  2  Q4X0H4_ASPFU            Q4x0h4 aspergillus
    26    1146   44.3    549  2  Q2UIS5_ASPOR            Q2uis5 aspergillus
    27  1131.5   43.8    492  2  Q7SDJ6_NEUCR            Q7sdj6 neurospora
    28  1115.5   43.2    568  2  Q4WI35_ASPFU            Q4wi35 aspergillus
    29  1098.5   42.5    521  2  Q5B4M3_EMENI            Q5b4m3 aspergillus
    30  1090.5   42.2    559  2  Q5AZF6_EMENI            Q5azf6 aspergillus
    31    1088   42.1    552  2  Q5B822_EMENI            Q5b822 aspergillus
    32    1062   41.1    561  2  Q4WFV4_ASPFU            Q4wfv4 aspergillus
    33  1061.5   41.1    532  2  Q2KHC0_MAGGR            Q2khc0 magnaporthe
    34    1057   40.9    532  2  Q55S33_CRYNE            Q55s33 cryptococcu
    35    1057   40.9    532  2  Q5KGI6_CRYNE            Q5kgi6 cryptococcu
    36    1001   38.7    533  2  Q7S4K0_NEUCR            Q7s4k0 neurospora
    37     908   35.1    513  1  AMY3_SCHPO              O14154 schizosacch
    38   903.5   35.0    572  2  Q55KB2_CRYNE            Q55kb2 cryptococcu
    39   902.5   34.9    572  2  Q5K993_CRYNE            Q5k993 cryptococcu
    40     901   34.9    625  2  O74922_SCHPO            O74922 schizosacch
    41   852.5   33.0    564  1  AMY4_SCHPO              Q9y7s9 schizosacch
    42     845   32.7    460  2  Q4IG16_GIBZE            Q4ig16 gibberella
    43   837.5   32.4    561  2  Q5KPY6_CRYNE            Q5kpy6 cryptococcu
    44   835.5   32.3    600  2  Q2KEQ7_MAGGR            Q2keq7 magnaporthe
    45     832   32.2    460  2  Q3YBZ7_GIBMO            Q3ybz7 gibberella


                              ALIGNMENTS

RESULT 1
AMYA_ASPNG
ID   AMYA_ASPNG     STANDARD;      PRT;   484 AA.
AC   P56271;
DT   15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
DT   15-JUL-1998, sequence version 1.
DT   07-FEB-2006, entry version 34.
DE   Acid alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
OS   Aspergillus niger.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX   NCBI_TaxID=5061;
RN   [1]
RP   X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX   MEDLINE=91002514; PubMed=2207069;
RA   Boel E., Brady L., Brzozowski A.M., Derewenda Z., Dodson G.G.,
RA   Jensen V.J., Petersen S.B., Swift H., Thim L., Woldike H.F.;
RT   "Calcium binding in alpha-amylases: an X-ray diffraction study at 2.1-
RT   A resolution of two enzymes from Aspergillus.";
RL   Biochemistry 29:6244-6249(1990).
CC   -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-D-glucosidic
CC       linkages in oligosaccharides and polysaccharides.
CC   -!- COFACTOR: Binds 2 calcium ions per subunit. Calcium is inhibitory
```

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CC       at high concentrations.
CC   -!- SUBUNIT: Monomer.
CC   -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   PDB; 2AAA; X-ray; @=1-484.
DR   LinkHub; P56271; -.
DR   InterPro; IPR006589; Alp_amyl_cat_sub.
DR   InterPro; IPR006047; Alpha_amyl_cat.
DR   Pfam; PF00128; Alpha-amylase; 1.
DR   SMART; SM00642; Aamy; 1.
KW   3D-structure; Calcium; Carbohydrate metabolism; Glycoprotein;
KW   Glycosidase; Hydrolase; Metal-binding.
FT   CHAIN         1    484       Acid alpha-amylase.
FT                                /FTId=PRO_0000054289.
FT   ACT_SITE    206    206       Nucleophile.
FT   ACT_SITE    230    230       Proton donor.
FT   ACT_SITE    297    297
FT   METAL       121    121       Calcium 1.
FT   METAL       162    162       Calcium 1 (via carbonyl oxygen).
FT   METAL       175    175       Calcium 1.
FT   METAL       206    206       Calcium 2.
FT   METAL       210    210       Calcium 1 (via carbonyl oxygen).
FT   METAL       230    230       Calcium 2.
FT   CARBOHYD     24     24       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    157    157       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    197    197       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID     30     38
FT   DISULFID    150    164
FT   DISULFID    240    283
FT   DISULFID    440    475
FT   HELIX         3      6
FT   TURN          7      8
FT   STRAND       11     13
FT   HELIX        16     19
FT   TURN         22     23
FT   STRAND       26     26
FT   HELIX        32     34
FT   STRAND       36     36
FT   HELIX        42     47
FT   TURN         48     48
FT   HELIX        49     53
FT   TURN         54     56
FT   STRAND       59     62
FT   STRAND       66     68
FT   STRAND       73     73
FT   TURN         74     75
FT   STRAND       76     76
FT   STRAND       78     78
FT   TURN         79     80
FT   STRAND       81     81
FT   STRAND       83     90
FT   TURN         92     94
FT   HELIX        97    108
FT   TURN        109    111
FT   STRAND      113    118
FT   STRAND      121    122
FT   STRAND      125    127
FT   HELIX       129    131
FT   HELIX       134    136
FT   STRAND      137    139
FT   STRAND      142    142
FT   HELIX       143    145
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FT   STRAND      146    146
FT   STRAND      151    151
FT   TURN        155    156
FT   HELIX       158    163
FT   STRAND      164    167
FT   STRAND      169    173
FT   STRAND      175    176
FT   TURN        178    179
FT   STRAND      180    180
FT   HELIX       181    198
FT   TURN        199    199
FT   STRAND      202    206
FT   STRAND      208    208
FT   TURN        209    210
FT   STRAND      211    211
FT   HELIX       213    223
FT   TURN        224    224
FT   STRAND      225    229
FT   STRAND      234    234
FT   HELIX       236    244
FT   TURN        245    245
FT   STRAND      246    250
FT   HELIX       252    262
FT   STRAND      263    264
FT   TURN        265    266
FT   STRAND      267    267
FT   HELIX       269    282
FT   STRAND      284    284
FT   HELIX       286    288
FT   STRAND      289    291
FT   STRAND      293    293
FT   TURN        296    297
FT   STRAND      298    298
FT   HELIX       301    303
FT   TURN        304    304
FT   HELIX       308    320
FT   STRAND      321    328
FT   TURN        329    334
FT   TURN        339    343
FT   HELIX       347    350
FT   TURN        351    352
FT   TURN        354    355
FT   HELIX       357    375
FT   TURN        377    381
FT   STRAND      382    382
FT   STRAND      385    390
FT   TURN        391    392
FT   STRAND      393    400
FT   TURN        401    403
FT   STRAND      405    410
FT   STRAND      412    412
FT   TURN        414    415
FT   STRAND      416    416
FT   STRAND      419    423
FT   TURN        430    431
FT   STRAND      432    436
FT   TURN        437    438
FT   STRAND      439    444
FT   TURN        447    448
FT   STRAND      449    449
FT   STRAND      451    455
FT   TURN        457    458
FT   STRAND      461    465
FT   HELIX       466    469
FT   TURN        470    471
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